

FIG. 2

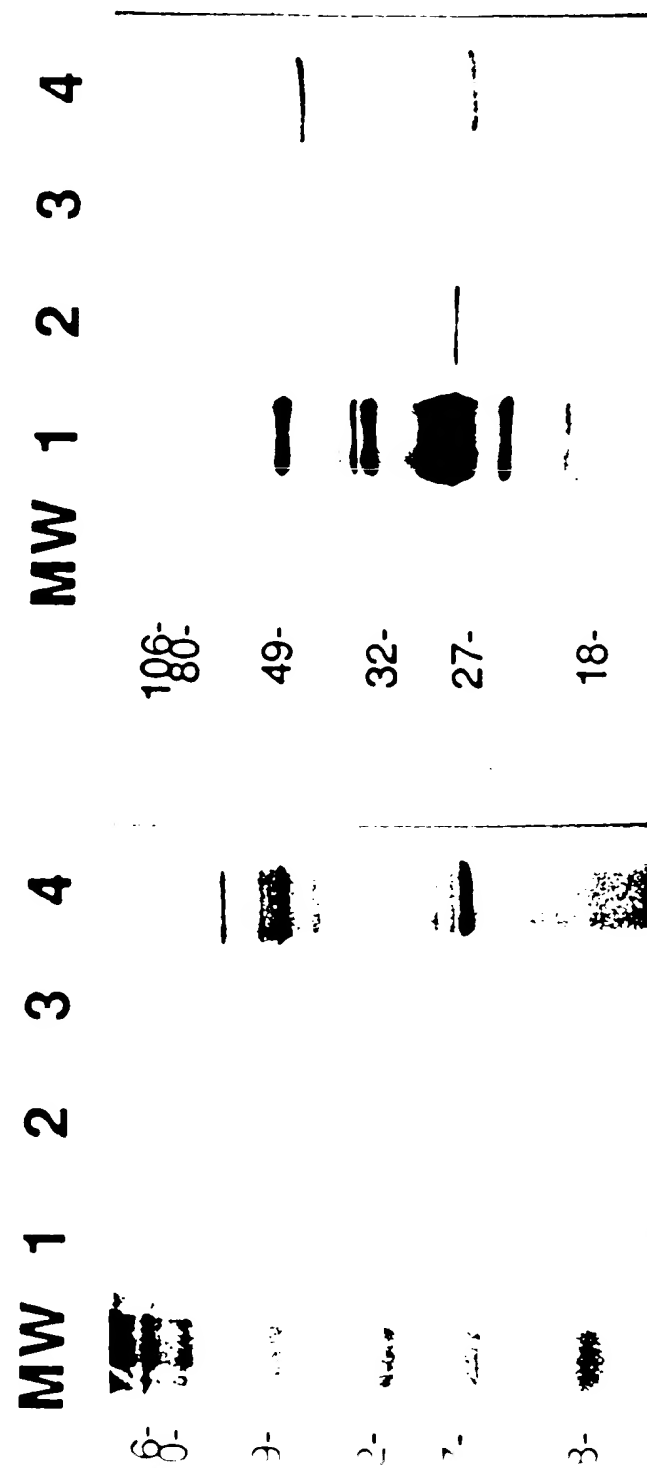


FIG. 3A

FIG. 3B

AA	CAAAATAAAAATTAATAATTATATATATTTTATGATAAATCACATATATTGAC	60
	-35	
TT	ATTGTTACTGTATGATACAGGCATAAGTACTTATTATTATTATAGATTGCAA	120
	+1	
	-10	
TT	CAATTATATTTTTCAAAGAGGAATGCTT ATG GAA TTC AAA AAG TTA CTT TAT	180
	SD Met Glu Phe Lys Lys Leu Tyr	8
	a SIGNAL PEPTIDE a a >	
TT	GGT TCA ATC GCA GGA ATT ACT TTA TTT TCC CCA ATT TTA ACA AGT GTC CAA GCA	240
Leu	Gly Ser Ile Ala Gly Ile Thr Leu Phe Ser Pro Ile Leu Thr Ser Val Gln Ala>	28
	a a a a SIGNAL PEPTIDE a a a a a a >	
AA	ATA AAT GTT AGT CAA CCA TCT AAT AAT GAA AGT AAT GTT ATT TCA CAG AAA AAA	300
Asn	Ile Asn Val Ser Gln Pro Ser Asn Asn Glu Ser Asn Val Ile Ser Gln Lys Lys>	48
	b b b b MATURE PEPTIDE b b b b b b b b >	
GA	ATT GAT AAT AGT CTA AAT CAG GAA AGT GCT CAA CTA TAT GCC TTG AAA GAA GAT	360
Gl	Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala Leu Lys Glu Asp>	68
	b b b b MATURE PEPTIDE b b b b b b b b >	
GT	GGA ACT GAG AAA GAA CAA TCA GTT AAT TCA GCA ATT TCA GCT GTT GAA AAT TTA	420
Val	Gly Thr Glu Lys Glu Gln Ser Val Asn Ser Ala Ile Ser Ala Val Glu Asn Leu>	88
	b b b b MATURE PEPTIDE b b b b b b b b >	

FIG. 4A

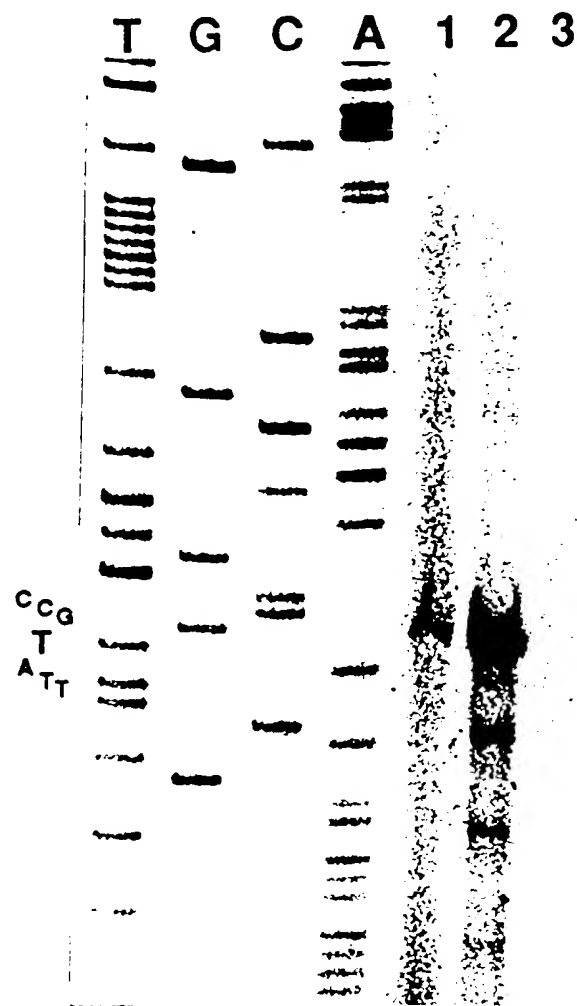


FIG. 5

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SUCAMP - MEFKLLYLTGSIAGITLSPILTSVQANQINVSQP-----SNNESNVIS -45
SAGCAMP -      :. :      :      :      :      :      :      :      :
      DQVTPQVVNVHNSNNQAQQMA -22

SUCAMP - QKKEEIDNSLNQESAQLYALKEDVKGTEKEQSVNSAISAVENLKTSLRAN -95
SAGCAMP -      :. :      :      :      :      :      :      :      :
      DQDSIQLRNIKDNVQGTDEKPVNEAITSVEKLTSLRAN -65

SUCAMP - PETIYDLNSIGTRVEAISDVIAIVFSTQQLTNKKVDQAHIDMGFAITKLL -145
SAGCAMP -      :. :      :      :      :      :      :      :      :
      SETVYDLNSIGSRVEALTDVIEAITFFSTQHLANKVSQANIDMGFGITKLIV -115

SUCAMP - IRIADPFASNESIKGQVEAVKQVQATVLTYPDLQPTDRATIYVKSCLDKL -195
SAGCAMP -      :. :      :      :      :      :      :      :      :
      IRILDPFASVDSIKAQVNDVKALEQKVLTYPDLKPTDRATIYTKSKLDKE -165

SUCAMP - IWQTRITRDQKVLNVKSFEVYHQLNKAITHAVGVQLNPTVTVAQVDQEIK -245
SAGCAMP -      :. :      :      :      :      :      :      :      :
      IWNTRFTRDKKVLNVKEFKVYNTLNKAITHAVGVQLNPNVTVQQVDQEIV -215

SUCAMP - VLQEALNTALQ -256
SAGCAMP -      :. :      :      :
      TLQAALQTALK -226

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FIG. 6

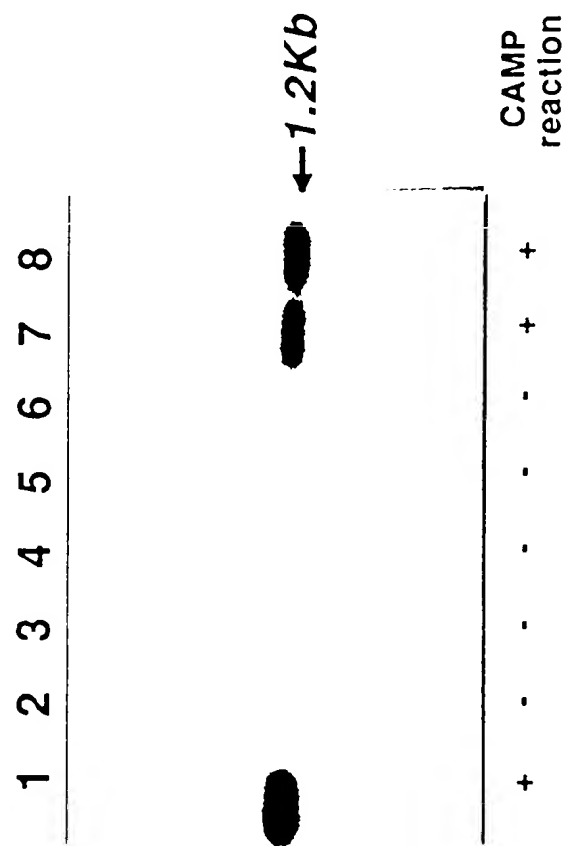


FIG. 7

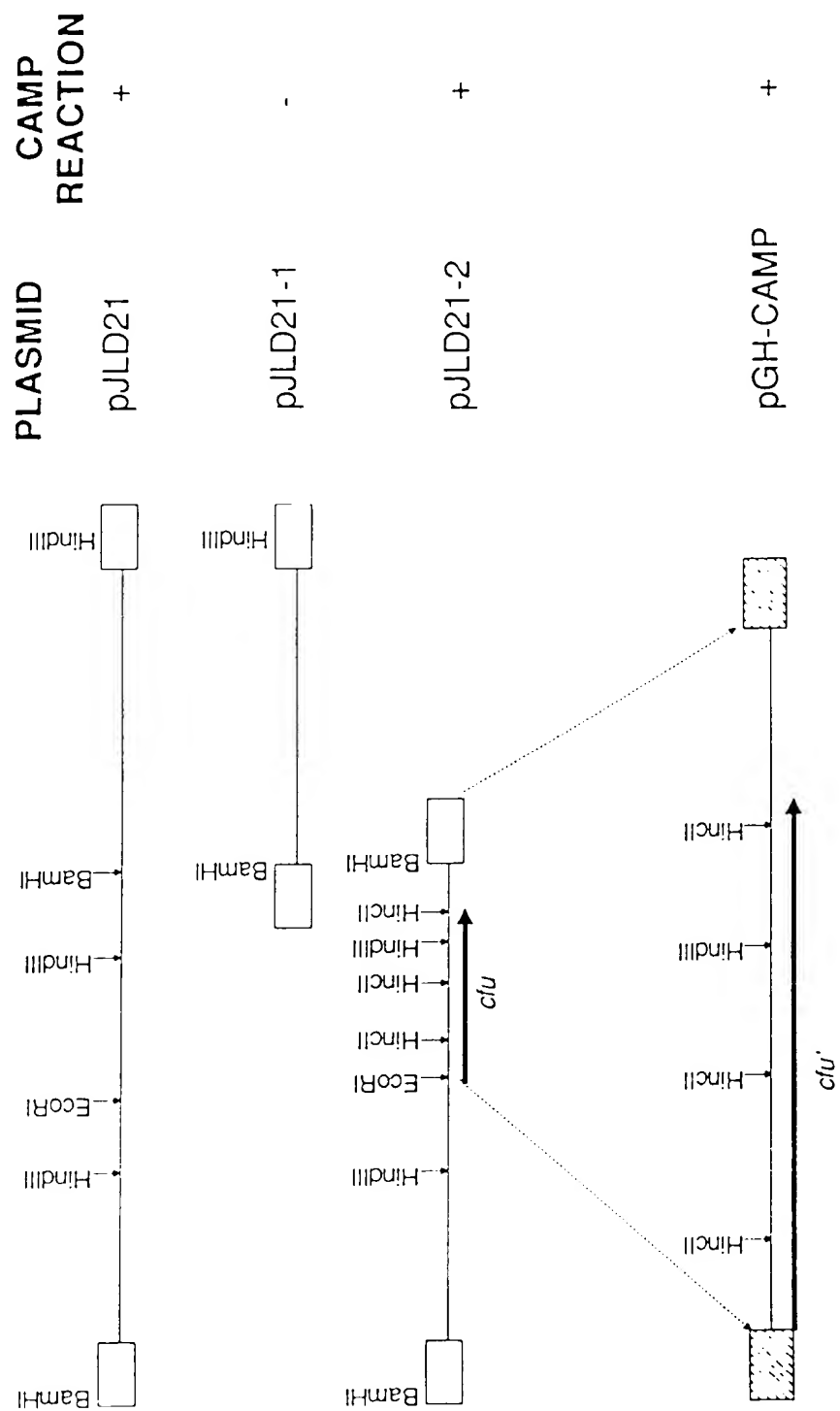


FIG. 8